

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5. (Canceled)

6. (Currently amended) The method of claim [[5]] 8, wherein the DNA methylation pattern for the test stem cell, stem cell tissue, or stem cell nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Canceled)

8. (Currently amended) ~~The method of claim 5, wherein the test cell, tissue, or nucleus is a stem cell~~ A method of identifying the differentiation state of a stem cell, stem cell tissue, or stem cell nucleus comprising:

obtaining a DNA methylation pattern for the stem cell, stem cell tissue, or stem cell nucleus, wherein the DNA methylation pattern for the stem cell, stem cell tissue, or stem cell nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state; and,

comparing the DNA methylation pattern for the stem cell, stem cell tissue, or stem cell nucleus with the differentiation state-specific DNA methylation pattern.

wherein the differentiation state of the stem cell, stem cell tissue, or stem cell nucleus is identified if the DNA methylation pattern of the stem cell, stem cell tissue, or stem cell nucleus matches the differentiation state-specific DNA methylation pattern.

9. (Currently amended) The method of claim [[5]] 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18. (Canceled)

19. (Previously presented) The method of claim 8, wherein the stem cell is an embryonic stem cell.

20. (Currently amended) The method of claim [[5]] 8, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is differentiated.

21. (Currently amended) The method of claim [[5]] 8, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is undifferentiated.

22. (Currently amended) A method of identifying a ~~test~~ stem cell, stem cell tissue, or stem cell nucleus, comprising:

obtaining a DNA methylation pattern for the ~~test~~ stem cell, stem cell tissue, or stem cell nucleus, wherein the DNA methylation pattern for the ~~test~~ stem cell, stem cell tissue, or stem cell nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of cell, tissue, or nucleus; wherein the one or more known types of cell, tissue, or nucleus is selected from undifferentiated embryonic stem cell, differentiated embryonic stem cell, undifferentiated trophoblast stem cell, and differentiated trophoblast stem cell, ~~kidney, placenta, brain, and sperm~~; and,

comparing the DNA methylation pattern for the ~~test~~ stem cell, stem cell tissue, or stem cell nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known cell, tissue, or nucleus to permit identification of the stem cell, stem cell

tissue, or stem cell nucleus as one of the known types of stem cell,
stem cell tissue, or stem cell nucleus;

wherein a match to the cell-, tissue-, or nucleus-specific
DNA methylation pattern of the undifferentiated embryonic
stem cell identifies the ~~test~~ stem cell, stem cell tissue, or
stem cell nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific
DNA methylation pattern of the differentiated embryonic
stem cell identifies the ~~test~~ stem cell, stem cell tissue, or
stem cell nucleus as differentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific
DNA methylation pattern of the undifferentiated
trophoblast stem cell identifies the ~~test~~ stem cell, stem cell
tissue, or stem cell nucleus as undifferentiated trophoblast
stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific
DNA methylation pattern of the differentiated trophoblast
stem cell identifies the ~~test~~ stem cell, stem cell tissue, or
stem cell nucleus as differentiated trophoblast stem cell.

~~wherein a match to the cell-, tissue-, or nucleus-specific~~
~~DNA methylation pattern of the kidney identifies the test~~
~~cell, tissue, or nucleus as kidney;~~

~~wherein a match to the cell-, tissue-, or nucleus-specific~~
~~DNA methylation pattern of the placenta identifies the test~~
~~cell, tissue, or nucleus as placenta;~~

~~wherein a match to the cell, tissue, or nucleus specific
DNA methylation pattern of the brain identifies the test
cell, tissue, or nucleus as brain; and,~~

~~wherein a match to the cell, tissue, or nucleus specific
DNA methylation pattern of the sperm identifies the test
cell, tissue, or nucleus as sperm.~~

23. (Previously presented) The method of claim 22, wherein the DNA
methylation patterns are obtained by generating RLGS profiles.